



H 11

1

SEQUENCE LISTING

<110> Kindsvogel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

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<221> CDS

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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
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ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
60 65 70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac 294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
75 80 85

ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc 342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
90 95 100

cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act 390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr
105 110 115

acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att 438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
120 125 130 135

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cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly 140 145 150	486
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu 155 160 165	534
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln 170 175 180	582
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly 185 190 195	630
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr 200 205 210 215	678
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ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu 315 320 325	1014
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3

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His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser		
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Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met		
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Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	Leu	His	Ser	Gly	Glu	Glu	Gly		
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Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro		
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tgt	tcc	ccc	tcg	gac	caa	ggt	cca	agt	ccc	tgg	ggc	ctg	ctg	gag	tcc	1638	
Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser		
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ctt	gtg	tgt	ccc	aag	gat	gaa	gcc	aag	agc	cca	gcc	cct	gag	acc	tca	1686	
Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys	Ser	Pro	Ala	Pro	Glu	Thr	Ser		
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<212> PRT

<213> Homo sapien

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Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
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Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
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Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
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Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
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Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys
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Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr
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Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe
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His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln
			165				170					175			
Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr
			180				185					190			
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp
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Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
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Arg	Thr	Trp	Thr	Tyr	Ser	Phe	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly
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Phe	Leu	Val	Ala	Val	Leu	Cys	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys
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Pro	Pro	Ala	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
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Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp
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Leu	Ser	Gly	Pro	Ser	Ser	Leu	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile
			290				295					300			
Arg	Val	Ser	Gly	Pro	Arg	Glu	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser
			305				310					315			320
Leu	Ser	Glu	Ile	Thr	Tyr	Leu	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln
			325				330					335			
Pro	Ser	Asn	Val	Pro	Pro	Pro	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala
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Pro	Asn	Ala	Ala	Pro	Glu	Val	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	val
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Thr	Pro	Glu	Ala	Gln	Phe	Pro	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys
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Val	Gln	Pro	Ser	Ser	Tyr	Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro
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Pro	Ser	Tyr	Gly	Val	Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr
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Gly	Thr	Leu	Ser	Ser	Pro	Lys	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln
			420				425					430			
Lys	Glu	Pro	Pro	Ala	Gly	Ser	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln
			435				440					445			
Glu	Val	Thr	Ser	Leu	Ala	Met	Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu
			450				455					460			
His	Gln	Pro	Leu	Gly	Ile	Cys	Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val
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Leu	His	Ser	Gly	Glu	Glu	Gly	Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	Leu
			485				490					495			
Pro	Leu	Leu	Ser	Ser	Val	Gln	Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro
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Leu	Gln	Pro	Pro	Ser	Gly	Pro	Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser
			515				520					525			
Pro	Trp	Gly	Leu	Leu	Glu	Ser	Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys
			530				535					540			
Ser	Pro	Ala	Pro	Glu	Thr	Ser	Asp	Leu	Glu	Gln	Pro	Thr	Glu	Leu	Asp
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Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
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35 40 45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
50 55 60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65 70 75 80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
85 90 95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
100 105 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
115 120 125
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
130 135 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145 150 155 160
His Leu Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
165 170 175
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Thr Trp Thr
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<212> PRT
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<213> Homo sapiens

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acccctgagg	tcacatgcgt	ggtgggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aacttgtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccaggaa	ctggctgaat	300
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Leu	Met	Gly	Thr	Leu	Ala	Thr	Ser	Cys	Leu	Leu	Leu	Leu	Ala	Leu	Leu	
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gta	cag	gga	gga	gca	gct	gcg	ccc	atc	agc	tcc	cac	tgc	agg	ctt	gac	149
Val	Gln	Gly	Gly	Ala	Ala	Ala	Pro	Ile	Ser	Ser	His	Cys	Arg	Leu	Asp	
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Lys	Ser	Asn	Phe	Gln	Gln	Pro	Tyr	Ile	Thr	Asn	Arg	Thr	Phe	Met	Leu	
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gct	aag	gag	gct	ttg	gct	aat	aac	aca	gac	gtt	cgt	ctc	att		245	
Ala	Lys	Glu	Ala	Ser	Leu	Ala	Asp	Asn	Asn	Thr	Asp	Val	Arg	Leu	Ile	
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Gly	Glu	Lys	Leu	Phe	His	Gly	Val	Ser	Met	Ser	Glu	Arg	Cys	Tyr	Leu	
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atg	aag	cag	gtg	ctg	aac	ttc	acc	ctt	gaa	gaa	gtg	ctg	ttc	cct	caa	341
Met	Lys	Gln	Val	Leu	Asn	Phe	Thr	Leu	Glu	Glu	Val	Leu	Phe	Pro	Gln	
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Ser	Asp	Arg	Phe	Gln	Pro	Tyr	Met	Gln	Glu	Val	Val	Pro	Phe	Leu	Ala	
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His	Ile	Gln	Arg	Asn	Val	Gln	Lys	Leu	Lys	Asp	Thr	Val	Lys	Lys	Leu	
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 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
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 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC28590

<400> 9
ttgggtacct ctgcaatggc cgccctgcag aatatct

36

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC28580

<400> 10
ttgggatcca atgcaggcat ttctcagaga cat

33

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC14666

<400> 11
agccaccaag atgactga 18

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC14742

<400> 12
tgcatttgtt aggtgcgggtt ga 22

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 13
His His His His His His 1 5

<210> 14
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC29239

<400> 14
gaggccggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 15
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29232

<400> 15
cgactgactc gagtcagtga tggtgatggt gatggccacc tgatcctta cccggagaca 60
gggag 65

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39319

<400> 16
atcggaaattc gcagaaggcca tggcgtggag ccttgggg 37

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC39325

<400> 17
 cagttggatcc ggaggggacc gtttcgtc 28

<210> 18
 <211> 660
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(660)

<400> 18	48
atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca	
Met Ala Trp Ser Leu Gly Ser Ile Leu Gly Gly Cys Leu Leu Val Ser	
1 5 10 15	
gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	
Ala Leu Gly Met Val Pro Pro Glu Asn Val Arg Met Asn Ser Val	
20 25 30	
aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly	
35 40 45	
aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp	
50 55 60	
aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser	
65 70 75 80	
aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu	
85 90 95	
cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile	
100 105 110	
att gga ccc cct gga atgcaa gta gaa gta ctt gat gat tct tta cat	
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His	
115 120 125	
atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act	
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr	
130 135 140	
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa	
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys	
145 150 155 160	
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag	
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu	
165 170 175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga	
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg	
180 185 190	

ggg ttt ctt cct gat cg_g aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 19

<211> 220

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38931

<400> 20

acaagccgc gggaggag

18

<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39042

<400> 21

ctgactcgag tcagtgtatgg ttagtgtat ggccacctga tccggAACCA cgccggAACCA 60
 gtttacccgg agacaggag ag 82

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<210> 22  
<211> 1428  
<212> DNA  
<213> Artificial Sequence
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<220>
<221> CDS
<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused to IgGg1 with a 6-HIS tag

```

<400> 22
atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
   1           5           10          15

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gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
          20           25           30

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aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc 240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag 288
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att 336
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat 384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190

ggg ttt ctt cct gat cg^g aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg 672
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220

12

ggg tgc ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro 225 230 235 240	720
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe 245 250 255	768
ccc cca aaa ccc aag gac acc ctc atg atc tcc cg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val 260 265 270	816
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 275 280 285	864
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 290 295 300	912
cg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr 305 310 315 320	960
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val 325 330 335	1008
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala 340 345 350	1056
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg Lys Gly Gln Pro Arg Glu Phe Gln Val Tyr Thr Ile Pro Pro Ser Arg 355 360 365	1104
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly 370 375 380	1152
tcc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg Phe Tyr Pro Ser Asp Ile Ala Val Glu Tyr Glu Ser Asn Gly Gln Pro 385 390 395 400	1200
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser 405 410 415	1248
tcc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 420 425 430	1296
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His 435 440 445	1344
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg 450 455 460	1392
ggt tcc gga tca ggt ggc cat cac cat cac cat cac Gly Ser Gly Ser Gly Gly His His His His His His 465 470 475	1428

<210> 23

<211> 476

<212> PRT

<213> Homo sapiens

<400> 23
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 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
 225 230 235 240
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
 245 250 255
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 275 280 285
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29328

<400> 24
tcagaggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 25
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29231

<400> 25
cgactgactc gagctactcc ataggcatat actcgccacc tgatcctta cccggagaca 60
gggag 65

<210> 26
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39335

<400> 26
atcggaaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC28981

<400> 27
tttgggctcc ctgagctctg gtggaa 26

<210> 28
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39043

<400> 28
ctgactcgag ctactccata ggcataatact cgccacctga tccggAACCA cgCGGAACCA 60
gtttacccgg agacagggag 80

<210> 29
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> hzcytor11 extracellular cytokine binding domain
fused to IgG1 with a Glu-Glu tag

<221> CDS
<222> (1)...(1452)

<400> 29
atg agg acg ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac 48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His

1	5	10	15	15	
gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg aaa ttc cag tcc Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser	20	25		30	96
agc aac ttt gaa aac atc ctg acg tgg gac agc ggg cca gag ggc acc Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr	35	40		45	144
cca gac acg gtc tac agc atc gag tat aag acg tac gga gag agg gac Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp	50	55		60	192
tgg gtg gca aag aag ggc tgt cag cggtt acc cgg aag tcc tgc aac Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn	65	70		75	240
ctg acg gtg gag acg ggc aac ctc acg gag ctc tac tat gcc agg gtc Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val	85	90		95	288
acc yct gtc agt gcg gga ggc cggtt tca gcc acc aag atg act qac agg Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg	100	105		110	336
ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys	115	120		125	384
atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr	130	135		140	432
cca atc cgt gca ggc gat ggc cac cggtt cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe	145	150		155	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln	165	170		175	528
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr	180	185		190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp	195	200		205	624
gcc aag gag agt ggc ccc tac atg tgc cga gtg aag aca ctg cca gag Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp	210	215		220	672
cggtt acc gca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser	225	230		235	720
tca gac aaa act cac aca tgc cca ccgtt gtc cca gca cct gaa gcc gag Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu	245	250		255	768
ggg gca ccgtt tca gtc ttc ctc ttc ccc cca aaa ccc aag gag acc ctc Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	260	265		270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	275	280		285	864

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
290 295 300	
gtg cat aat gcc aag aca aag ccg cgag gag cag tac aac agc acg	960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
305 310 315 320	
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
325 330 335	
gcc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc	1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser	
340 345 350	
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
355 360 365	
gtg tac acc ctg ccc cca tcc cggt gat gag ctg acc aag aac cag gtc	1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val	
370 375 380	
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg	1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
385 390 395 400	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct	1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
405 410 415	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
420 425 430	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg	1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
435 440 445	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg	1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
450 455 460	
tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat	1440
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Glu Tyr	
465 470 475 480	
atg cct atg gag	1452
Met Pro Met Glu	

<210> 30
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide encoded by the hzcytor11 extracellular cytokine binding domain fused to IgG1 with a Glu-Glu tag of SEQ ID NO: 29

<400> 30
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
1 5 10 15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
20 25 30

Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480
 Met Pro Met Glu

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<212> DNA

<213> Artificial Sequence

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<400> 31

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<210> 33

<211> 199

<212> PRT

<213> Homo sapiens

<400> 33

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Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
					20				25					30	
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
					35				40					45	
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
					50				55					60	
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
					65				70					80	
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
					85				90					95	
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
					100				105					110	
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
					115				120					125	
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
					130				135					140	
Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	Val	Leu	Arg
					145				150					160	
Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	Gly	Phe	Leu
					165				170					175	
Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	Cys	Glu	Gln
					180				185					190	
Thr	Thr	His	Asp	Glu	Thr	Val									
					195										

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<211> 211

<212> PRT

<213> Homo sapiens

<400> 34

Ser	Asp	Ala	His	Gly	Thr	Glu	Leu	Pro	Ser	Pro	Pro	Ser	Val	Trp	Phe
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Glu	Ala	Glu	Phe	Phe	His	His	Ile	Leu	His	Trp	Thr	Pro	Ile	Pro	Asn
					20				25					30	
Gln	Ser	Glu	Ser	Thr	Cys	Tyr	Glu	Val	Ala	Leu	Leu	Arg	Tyr	Gly	Ile
					35				40					45	
Glu	Ser	Trp	Asn	Ser	Ile	Ser	Asn	Cys	Ser	Gln	Thr	Leu	Ser	Tyr	Asp
					50				55					60	
Leu	Thr	Ala	Val	Thr	Leu	Asp	Leu	Tyr	His	Ser	Asn	Gly	Tyr	Arg	Ala
					65				70					80	
Arg	Val	Arg	Ala	Val	Asp	Gly	Ser	Arg	His	Ser	Asn	Trp	Thr	Val	Thr
					85				90					95	
Asn	Thr	Arg	Phe	Ser	Val	Asp	Glu	Val	Thr	Leu	Thr	Val	Gly	Ser	Val
					100				105					110	
Asn	Leu	Glu	Ile	His	Asn	Gly	Phe	Ile	Leu	Gly	Lys	Ile	Gln	Leu	Pro
					115				120					125	

19

Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
130 135 140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145 150 155 160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
165 170 175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
180 185 190
Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
195 200 205
Thr Arg Gln
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<213> Homo sapiens

<400> 35

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
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Thr Asn Met Lys His Ile Leu Met Trp Ser Pro Val Ile Ala Pro Gly
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Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
35 40 45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
50 55 60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65 70 75 80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
85 90 95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
100 105 110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
115 120 125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
130 135 140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145 150 155 160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
165 170 175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
180 185 190
Glu Cys Val Glu Val Gln Gly Glu Ala
195 200